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OM protein - protein search, using sw model

Run on: September 29, 2004, 16:40:30 ; Search time 120 Seconds
(without alignments)
42.382 Million cell updates/sec

Title: US-09-847-946b-131

Perfect score: 105

Sequence: 1 RRMKKKKTALDWSLQTE 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	18	5	AAM48628
2	105	100.0	18	5	AAM48628
3	105	100.0	18	6	ADA61904
4	105	100.0	18	6	ADA61905
5	105	100.0	18	6	ADA61922
6	105	100.0	28	5	AB08740
7	105	100.0	28	5	AAM48523
8	105	100.0	28	6	ABU08434
9	105	100.0	28	6	ADA61791
10	105	100.0	28	6	ADA61936
11	77	73.3	28	5	AB08741
12	77	73.3	28	5	AAM48524
13	77	73.3	28	6	ABU08435
14	77	73.3	28	6	ADA61792
15	77	73.3	28	6	ADA61937
16	76	72.4	18	5	AAM48632
17	76	72.4	18	5	AAM48633
18	76	72.4	18	6	ADA61924
19	76	72.4	18	6	ADA61908
20	76	72.4	18	6	ADA61909
21	72	68.6	22	5	AAM48630
22	72	68.6	22	5	AAM48631
23	72	68.6	22	6	ADA61907
24	72	68.6	22	6	ADA61923
25	72	68.6	22	6	ADA61906

ALIGNMENTS

RESULT 1

AAM48628
ID AAM48628 standard; peptide; 18 AA.

XX AC AAM48628;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 131.

XX
KW Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.

OS WO200183554-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

PR 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

PA (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV VALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.

PS Claim 12; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

26	70	66.7	13	5	AAM48640
27	70	66.7	13	5	AAM48641
28	70	66.7	13	6	ADA61916
29	70	66.7	13	6	ADA61927
30	70	66.7	13	6	ADA61928
31	70	66.7	12	5	AAM48634
32	70	66.7	22	5	AAM48635
33	70	66.7	22	6	ADA61911
34	70	66.7	22	6	ADA61910
35	70	66.7	22	6	ADA61925
36	68	64.8	22	5	AAM48637
37	68	64.8	22	5	AAM48636
38	68	64.8	22	6	ADA61912
39	68	64.8	22	6	ADA61926
40	68	64.8	22	6	ADA61913
41	64	61.0	11	5	AAM48525
42	64	61.0	11	5	AAM48506
43	64	61.0	11	6	ADA61801
44	64	61.0	36	5	AAM48652
45	64	61.0	36	6	ABU08436

Thu Sep 30 09:09:14 2004

us-09-847-946b-131.rag

antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and anti-allergic activity. The compounds act as selective inhibitors of cytokine-mediated NF-kappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

SQ Sequence 18 AA;

Query Match 100.0%; Score 105; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLOTE 18
| | | | | | | | | | | | | | | | | |
Db 1 RRMKWKKTALDWSWLOTE 18

RESULT 2

ID AAM48629 standard; peptide; 18 AA.

AC AAM48629;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 132.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYUA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.

XX Claim 12; Page 63; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and anti-allergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IkappaB. The compounds are useful
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis

SQ Sequence 18 AA;

Query Match 100.0%; Score 105; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLOTE 18
| | | | | | | | | | | | | | | | | |
Db 1 RRMKWKKTALDWSWLOTE 18

RESULT 3

ID ADA61904 standard; peptide; 18 AA.

AC ADA61904;

DT 20-NOV-2003 (first entry)

DE NFKB essential modulator (NEMO) binding peptide #104.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
XX antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis; autoimmune disease;
KW inflammatory bowel disease; sepsis; vasculitis;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.

OS Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

PF 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (WAYM/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Claim 12; Page 24; 37pp; English.
XX
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
XX Sequence 18 AA;
SQ
Query Match 100.0%; Score 105; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMKKKKTALDWSWLOTE 18
DB 1 RRMKKKKTALDWSWLOTE 18
|||||
RESULT 4
ADA61905
ID ADA61905 standard; peptide; 18 AA.
XX
XX ADA61905;
XX
XX 20-NOV-2003 (first entry)
XX
XX NFkB essential modulator (NEMO) binding peptide #105.
DE
XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutropenic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
XX Unidentified.
OS
XX US2003054999-A1.
PN
XX 20-MAR-2003.
PD
XX
XX 02-MAY-2001; 2001US-00847946.
PF
XX
XX 20-MAR-2003.
PD
XX
XX 02-MAY-2001; 2001US-00847946.
PF
XX
XX 02-MAY-2000; 2000US-0201261P.
PR
XX
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR
XX
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.

XX Claim 12; Page 24; 37pp; English.
XX
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
XX Sequence 18 AA;
SQ
Query Match 100.0%; Score 105; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMKKKKTALDWSWLOTE 18
DB 1 RRMKKKKTALDWSWLOTE 18
|||||
RESULT 5
ADA61922
ID ADA61922 standard; peptide; 18 AA.
XX
XX ADA61922;
XX
XX 20-NOV-2003 (first entry)
XX
XX NFkB essential modulator (NEMO) binding peptide #122.
DE
XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutropenic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
XX Unidentified.
OS
XX US2003054999-A1.
PN
XX 20-MAR-2003.
PD
XX
XX 02-MAY-2001; 2001US-00847946.
PF
XX
XX 02-MAY-2000; 2000US-0201261P.
PR
XX
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR
XX
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Claim 13; Page 24; 37pp; English.
XX
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
CC cancer, comprises a membrane translocation domain and a NEMO binding
CC sequence.

CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 105; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 3e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18

DB 1 RRMKWKKTALDWSWLQTE 18

RESULT 6

ID ABB08740 standard; peptide; 28 AA.

XX ABB08740;

DT 14-JUN-2002 (first entry)

DE IKKbeta NEMO binding domain peptide SEQ ID NO 18.

XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; NBD; NF-kappaB; NF-kB;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer.

XX Homo sapiens.

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US040654.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (UYA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain.

XX Claim 23; Fig 5; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound (ABB08725-
 CC ABB08742) comprising at least one NEMO binding domain (ABB77313). The
 CC compound has acts through selective inhibition of cytokine-mediated NF-kB
 CC activation by blocking the interaction of NEMO with IKKbeta at the NEMO
 CC binding domain. Blockage of IKKbeta-NEMO interaction results in
 CC inhibition of IKKbeta kinase activation and subsequent decreased
 CC phosphorylation of IkappaB. The compound may also act (directly or
 CC indirectly) by blocking the recruitment of leukocytes into sites of acute
 CC and chronic inflammation, by down-regulating the expression of E-selectin

CC on leukocytes or by blocking osteoclast differentiation. The compound is
 CC useful in treating NF-kB mediated conditions, where the condition is an
 CC inflammatory disorder, an autoimmune disease, transplant rejection,
 CC osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
 CC infection or ataxia telangiectasia. The inflammatory disorder is asthma,
 CC allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
 CC psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
 CC inflammatory bowel disease, chronic obstructive pulmonary disease,
 CC vasculitis and bursitis. The inflammatory disorder may also be
 CC dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
 CC and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of the NEMO
 CC binding domain of IKKbeta

XX Sequence 28 AA;

Query Match 100.0%; Score 105; DB 5; Length 28;

Best Local Similarity 100.0%; Pred. No. 4.7e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18

DB 11 RRMKWKKTALDWSWLQTE 28

RESULT 7

ID AAM48523 standard; peptide; 28 AA.

XX AAM48523;

XX 20-MAR-2002 (first entry)

XX NBD peptide SEQ ID NO 18.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiarteriosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO binding domain.

Claim 23; Fig 5; 82pp; English.

The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprising contacting a cell with an anti-inflammatory compound (ABB08725-ABB08742) comprising at least one NEMO binding domain (ABB77313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO interaction results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkkappaB. The compound may also act (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory bowel disease, chronic obstructive pulmonary disease, vasculitis and bursitis. The inflammatory disorder may also be dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus and spondylarthritis. Also for Crohn's disease, ulcerative colitis, polyoma, scleroderma, Wegner's granulomatosis, temporal arteritis, cryoglobulinemia or multiple sclerosis. For chronic viral infections caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, sunburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying anti-inflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKbeta

Sequence 28 AA;

Query Match 73.3%; Score 77; DB 5; Length 28;
Best Local Similarity 88.9%; Pred. No. 0.00045;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18
Db 11 RRMKWKKTALDASALQTE 28

RESULT 12
AA048524
ID AAM48524 standard; peptide; 28 AA.

XX AAM48524;

XX 20-MAR-2002 (first entry)

DE NBD peptide SEQ ID NO 19.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS Synthetic.

XX WO200183554-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014346.
XX 02-MAY-2000; 2000US-0201261P.
XX 22-AUG-2000; 2000US-00643260.
XX (PRAE-) PRACIS PHARM INC.
XX (UYVA) UNIV YALE.
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.

Example 5; Fig 5; 88pp; English.

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, cytostatic, antipsoriatic, immunosuppressive, dermatological, neuroprotective, neurotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IkappaB kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 28 AA;

Query Match 73.3%; Score 77; DB 5; Length 28;
Best Local Similarity 88.9%; Pred. No. 0.00045;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18
Db 11 RRMKWKKTALDASALQTE 28

RESULT 13
ABU08435
ID ABU08435 standard; peptide; 28 AA.
XX ABU08435;

XX 12-JUN-2003 (first entry)

XX Human mutant NEMO binding site (NBD) peptide.
XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
XX nuclear factor-kappaB induction; inflammatory disorder;
XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX atherosclerosis; viral infection; Ataxia telangiectasia;
XX transplantation detection; immunosuppressive; osteopathic; cytostatic;
XX neurotropic; neuroprotective; antiatherosclerotic; virucide; vasotropic;

KW antirheumatic; antiarthritic; mutant; mutein.

XX Homo sapiens.
OS Synthetic.

XX US2002156000-A1.

XX 24-OCT-2002.

XX 02-MAY-2001; 2001US-00847940.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (MAYM/) MAY M J.

XX (GHOS/) GHOSH S.

XX May MJ, Ghosh S;

XX WPI; 2003-209142/20.

XX Novel antiinflammatory peptide compounds comprising NEMO binding domain,
PT useful for modulating NF-kappaB induction in a cell and for treating NF-
PT kappaB-mediated inflammation disorders e.g., asthma, psoriasis,
PT vasculitis.

XX Claim 22; Fig 5A; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are found on
CC IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha)
CC proteins. The antiinflammatory compounds of the invention are useful for
CC modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where
CC the compounds are capable of blocking the interaction between one or more
CC IKKs such as IKKalpha or IKKbeta, and NEMO. The antiinflammatory compound
CC further comprises at least one membrane translocation domain. The
CC compounds are useful for treating inflammatory disorders, autoimmune
CC diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis,
CC viral infections, Ataxia telangiectasia, and for transplantation
CC detection. The compounds of the invention block NF-kappaB induction by
CC IKK but do not inhibit the basal activity of NF-kappaB. The present
CC sequence represents a human mutant NBD peptide

SQ Sequence 28 AA;

Query Match 73.3%; Score 77; DB 6; Length 28;
Best Local Similarity 88.9%; Pred. No. 0.00045;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLQTE 18

Db 11 RRMKWKKTALDASALQTE 28

RESULT 14

ADA61792

ID ADA61792 standard; peptide; 28 AA.

XX ADA61792;

XX 20-NOV-2003 (first entry)

XX IKKbeta NEMO binding domain (NBD) peptide mutant.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutrotropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator; mutant; mutein.

XX Synthetic.
OS Homo sapiens.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

XX (GHOS/) GHOSH S.

XX (FIND/) FINDEIS M A.

XX (PHIL/) PHILLIPS K.

XX (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.

XX Example 5; Page 19; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of a I kappa B kinase beta (IKKbeta) NEMO binding domain (NBD) mutant
CC used in to determine which residues in the NBD are important for binding
CC NEMO (necrosis factor kappa B essential modulator).

SQ Sequence 28 AA;

Query Match 73.3%; Score 77; DB 6; Length 28;
Best Local Similarity 88.9%; Pred. No. 0.00045;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLQTE 18

Db 11 RRMKWKKTALDASALQTE 28

RESULT 15

ADA61937

ID ADA61937 standard; peptide; 28 AA.

XX ADA61937;

XX 20-NOV-2003 (first entry)

XX IKKbeta NEMO binding domain (NBD) peptide mutant #2.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutrotropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator; mutant; mutein.

OS Synthetic.

OS Homo sapiens.
XX
PN US2003054999-A1.
XX
XX
PD 20-MAR-2003.
XX
PF 02-MAY-2001; 2001US-00847946.
XX
XX 02-MAY-2000; 2000US-0201261P.
XX
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
FI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.
DR
XX
XX
PT New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Example 5; Fig 5A; 37pp; English.
PS
XX
XX The invention describes an anti-inflammatory compound comprising (i). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of a I kappa B kinase beta (IKKbeta) NEMO binding domain (NBD) mutant
CC used in to determine which residues in the NBD are important for binding
CC NEMO (necrosis factor kappa B essential modulator).
XX
SQ Sequence 28 AA;
Query Match 73.3%; Score 77; DB 6; Length 28;
Best Local Similarity 88.9%; Pred. No. 0.00045;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 RRMKKKTALDWSLQTE 18
Db 11 RRMKKKTALDASALQTE 28
|||||
|||||

Search completed: September 29, 2004, 16:53:49
Job time : 121 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 16:51:46 ; Search time 32 Seconds
(without alignments)
29.040 Million cell updates/sec

Title: US-09-847-946B-131
Perfect score: 105
Sequence: 1 RRMKWKKTALDWSWLQTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	61.0	756	2	US-08-887-518-4
2	64	61.0	756	2	US-09-023-321-4
3	64	61.0	756	2	US-08-890-853-2
4	64	61.0	756	2	US-09-032-475-4
5	64	61.0	756	2	US-09-099-125A-2
6	64	61.0	756	2	US-09-039-124A-2
7	64	61.0	756	3	US-09-032-476-2
8	64	61.0	756	3	US-08-890-854-2
9	64	61.0	756	3	US-09-023-324-2
10	64	61.0	756	3	US-09-168-629-15
11	64	61.0	756	3	US-09-910-820-9
12	64	61.0	756	4	US-09-109-886-2
13	64	61.0	756	4	US-09-844-908-9
14	64	61.0	756	4	US-09-868-758-4
15	48	45.7	10	2	US-08-637-759B-255
16	48	45.7	10	3	US-08-871-355A-255
17	48	45.7	10	4	US-09-201-945-255
18	48	45.7	73	4	US-09-216-393B-69
19	47.5	45.2	154	4	US-09-252-991A-17804
20	47	44.8	73	4	US-09-216-393B-106
21	45	42.9	439	4	US-09-172-952-14
22	44.5	42.4	786	4	US-09-543-681A-6650
23	44	41.9	21	4	US-08-610-220B-11
24	44	41.9	24	4	US-09-419-826-34
25	44	41.9	34	4	US-09-347-504-79
26	44	41.9	34	4	US-10-161-499-79
27	44	41.9	380	3	US-09-150-133-9

28	44	41.9	380	3	US-09-150-141-9	Sequence 9, Appli
29	44	41.9	380	3	US-09-374-493-9	Sequence 9, Appli
30	44	41.9	380	3	US-09-374-824-9	Sequence 9, Appli
31	44	41.9	380	3	US-09-374-492-9	Sequence 9, Appli
32	44	41.9	380	4	US-09-785-343-9	Sequence 2, Appli
33	43	41.0	27	4	US-09-040-725A-2	Sequence 2, Appli
34	43	41.0	242	4	US-09-345-236B-3	Sequence 3, Appli
35	43	41.0	299	4	US-09-252-991A-17878	Sequence 17878, A
36	43	41.0	426	4	US-09-252-991A-18298	Sequence 18298, A
37	43	41.0	915	4	US-09-252-991A-23779	Sequence 23779, A
38	42.5	40.5	788	4	US-09-489-039A-11122	Sequence 11122, A
39	42	40.0	27	3	US-09-051-934-51	Sequence 51, Appl
40	42	40.0	27	3	US-09-051-934-52	Sequence 52, Appl
41	42	40.0	93	4	US-09-489-039A-12879	Sequence 12879, A
42	42	40.0	158	4	US-09-252-991A-28238	Sequence 28238, A
43	42	40.0	160	2	US-08-726-306A-64	Sequence 64, Appl
44	42	40.0	594	4	US-09-489-039A-13933	Sequence 13933, A
45	42	40.0	616	3	US-09-136-574A-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-887-518-4
; Sequence 4, Application US/08887518
; Patent No. 5843721
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
US-08-887-518-4

Query Match 61.0%; Score 64; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TALDWSWLQTE 18
Db 735 TALDWSWLQTE 745

RESULT 2
US-09-023-321-4
; Sequence 4, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/023,321
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-023-321-4
Query Match 61.0%; Score 64; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TALDWSWLQTE 18
Db 735 TALDWSWLQTE 745
RESULT 3
US-08-890-853-2
; Sequence 2, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
US-09-023-321-4

US-09-032-475-4
; Sequence 4, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-4
Query Match 61.0%; Score 64; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TALDWSWLQTE 18
Db 735 TALDWSWLQTE 745
RESULT 4
US-09-032-475-4
; Sequence 4, Application US/09032475
; Patent No. 5854003
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Wu, Lin
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,475
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/887,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-032-475-4

Query Match 61.0%; Score 64; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||||
Db 735 TALDWSWLQTE 745

RESULT 5
US-09-099-125A-2
; Sequence 2, Application US/09099125A
; Patent No. 5916760
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US/09/099,125A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US/09/099,125A-2

Query Match 61.0%; Score 64; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||||
Db 735 TALDWSWLQTE 745

RESULT 6
US-09-099-124A-2
; Sequence 2, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Woronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US-09-099-124A-2

Query Match 61.0%; Score 64; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||||
Db 735 TALDWSWLQTE 745

RESULT 7
US-09-032-476-2
; Sequence 2, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-476-2

Query Match 61.0%; Score 64; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TALDWSWLQTE 18
| | | | | | | | | | | | | | | | | | | | | |
Db 735 TALDWSWLQTE 745

RESULT 8
US-08-890-854-2
Sequence 2, Application US/08890854
Patent No. 6235512
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-2

Query Match 61.0%; Score 64; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TALDWSWLQTE 18
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Db 735 TALDWSWLQTE 745

RESULT 9
US-09-023-324-2
Sequence 2, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-324-2

Query Match 61.0%; Score 64; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TALDWSWLQTE 18
| | | | | | | | | | | | | | | | | | | | | |
Db 735 TALDWSWLQTE 745

RESULT 10
US-09-168-629-15
Sequence 15, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-15

Query Match 61.0%; Score 64; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||
Db 735 TALDWSWLQTE 745

RESULT 11
US-08-910-820-9
; Sequence 9, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,820
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.413C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-910-820-9

Query Match 61.0%; Score 64; DB 3; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||
Db 735 TALDWSWLQTE 745

RESULT 12
US-09-109-986-2
; Sequence 2, Application US/09109986
; Patent No. 6479266

; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Cao, Zhaodan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-109-986-2

Query Match 61.0%; Score 64; DB 4; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||
Db 735 TALDWSWLQTE 745

RESULT 13
US-09-844-908-9
; Sequence 9, Application US/09844908
; Patent No. 6576437
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; APPLICANT: Zhu, Hengyi
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,908
FILING DATE: 27-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-844-908-3

Query Match 61.0%; Score 64; DB 4; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||||
Db 735 TALDWSWLQTE 745

RESULT 14

US-09-868-758-4
Sequence 4, Application US/09868758
Patent No. 6576439
GENERAL INFORMATION:
APPLICANT: Glaxo Wellcome KK
APPLICANT: Takemoto, Yoshihiro
APPLICANT: Sakai, Yutaka
APPLICANT: Hashimoto, Yasuhiro
TITLE OF INVENTION: IKK3
FILE REFERENCE: 9950986P
CURRENT APPLICATION NUMBER: US/09/868,758
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: GB 9828704.8
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 756
TYPE: PRT
ORGANISM: Homo sapiens
US-09-868-758-4

Query Match 61.0%; Score 64; DB 4; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TALDWSWLQTE 18
|||||
Db 735 TALDWSWLQTE 745

RESULT 15

US-08-637-759B-255
Sequence 255, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: REMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 255:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-255

Query Match 45.7%; Score 48; DB 2; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.72;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MKWKKTALDW 12
|.|||.|||
Db 1 MRWKKITLSW 10

Search completed: September 29, 2004, 16:57:41
Job time : 33 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 16:56:27 ; Search time 128 Seconds
(without alignments)
45.253 Million cell updates/sec

Title: US-09-847-946B-131

Perfect score: 105

Sequence: 1 RMKWKKTALDWSLQTE 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubaa/US09_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	18	10	US-09-847-946A-131
2	105	100.0	28	9	Sequence 131, App
3	105	100.0	28	9	Sequence 18, Appl
4	105	100.0	28	10	US-09-847-946A-18
5	77	73.3	28	12	US-10-602-303-2
6	77	73.3	28	9	Sequence 2, Appl
7	76	72.4	18	10	US-09-847-946A-19
8	76	72.4	18	10	US-09-847-946A-135
9	72	68.6	22	10	US-09-847-946A-136
10	72	68.6	22	10	US-09-847-946A-133
11	70	66.7	13	10	US-09-847-946A-134
12	70	66.7	13	10	US-09-847-946A-143
13	70	66.7	13	10	US-09-847-946A-144
14	70	66.7	22	10	US-09-847-946A-137
15	68	64.8	22	10	US-09-847-946A-138
			22	10	US-09-847-946A-139

16	66	62.9	12	10	US-09-847-946A-43	Sequence 43, Appl
17	64	61.0	11	10	US-09-847-946A-28	Sequence 28, Appl
18	64	61.0	11	10	US-09-847-946A-132	Sequence 132, App
19	64	61.0	11	10	US-09-847-946A-140	Sequence 140, App
20	64	61.0	222	9	US-09-771-161A-141	Sequence 141, App
21	64	61.0	756	9	US-09-796-872-15	Sequence 15, Appl
22	64	61.0	756	9	US-09-771-161A-232	Sequence 232, App
23	64	61.0	756	9	US-09-771-161A-908-9	Sequence 9, Appl
24	64	61.0	756	9	US-09-844-988-9	Sequence 9, Appl
25	64	61.0	756	14	US-10-243-408-2	Sequence 2, Appl
26	64	61.0	756	14	US-10-338-462-9	Sequence 9, Appl
27	64	61.0	756	15	US-10-408-636-4	Sequence 4, Appl
28	64	61.0	756	15	US-10-394-322A-33	Sequence 33, Appl
29	64	61.0	769	12	US-10-087-192-1758	Sequence 1758, App
30	61	59.1	11	10	US-09-847-946A-101	Sequence 101, App
31	60	57.1	11	10	US-09-847-946A-112	Sequence 112, App
32	59	56.2	10	10	US-09-847-946A-31	Sequence 31, Appl
33	59	56.2	10	10	US-09-847-946A-34	Sequence 34, Appl
34	59	56.2	11	10	US-09-847-946A-46	Sequence 46, Appl
35	56	53.3	10	10	US-09-847-946A-104	Sequence 104, App
36	56	53.3	10	10	US-09-847-946A-107	Sequence 107, App
37	55	52.4	9	10	US-09-847-946A-29	Sequence 29, Appl
38	55	52.4	9	10	US-09-847-946A-32	Sequence 32, Appl
39	55	52.4	10	10	US-09-847-946A-115	Sequence 115, App
40	55	52.4	10	10	US-09-847-946A-118	Sequence 118, App
41	55	52.4	11	10	US-09-847-946A-90	Sequence 90, Appl
42	54	51.4	9	10	US-09-847-946A-35	Sequence 35, Appl
43	54	51.4	9	10	US-09-847-946A-36	Sequence 36, Appl
44	54	51.4	10	10	US-09-847-946A-49	Sequence 49, Appl
45	54	51.4	10	10	US-09-847-946A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-09-847-946A-131
; Sequence 131, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hennig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: anti-inflammatory compound
US-09-847-946A-131

Query Match 100.0%; Score 105; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RMKWKKTALDWSLQTE 18
|||||
DB 1 RMKWKKTALDWSLQTE 18
|||||

GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat
; TITLE OF INVENTION: Treatment of Human Multiple Myeloma by Curcumin
; FILE REFERENCE: D6467
; CURRENT APPLICATION NUMBER: US/10/602,303
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US 60/390,926
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; OTHER INFORMATION: Cell-permeable NEMO (NF-B essential modifier;
; OTHER INFORMATION: also called IKK()-binding domain peptide
US-10-602-303-2

Query Match 100.0%; Score 105; DB 12; Length 28;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLQTE 18
Db 11 RRMKWKKTALDWSWLQTE 28

RESULT 5
US-09-847-940B-19
; Sequence 19, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19

Query Match 73.3%; Score 77; DB 9; Length 28;
Best Local Similarity 88.9%; Pred. No. 0.0034;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLQTE 18
Db 11 RRMKWKKTALDASALQTE 28

RESULT 6
US-09-847-946A-19
; Sequence 19, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A

US-09-847-940B-18
; Sequence 18, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-18

Query Match 100.0%; Score 105; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLQTE 18
Db 11 RRMKWKKTALDWSWLQTE 28

RESULT 3
US-09-847-946A-18
; Sequence 18, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18

Query Match 100.0%; Score 105; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWKKTALDWSWLQTE 18
Db 11 RRMKWKKTALDWSWLQTE 28

RESULT 4
US-10-602-303-2
; Sequence 2, Application US/10602303
; Publication No. US20040058021A1

FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19

Query Match 73.3%; Score 77; DB 10; Length 28;
Best Local Similarity 88.9%; Pred. No. 0.0034;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18
|||:|||||:|||||
Db 11 RRMKWKKTALDASALQTE 28

RESULT 7
US-09-847-946A-135
Sequence 135, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 135
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-135

Query Match 72.4%; Score 76; DB 10; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.0031;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18
|||:|||||:|||||
Db 1 RRRRRRTALDWSWLQTE 18

RESULT 8
US-09-847-946A-136
Sequence 136, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 136
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-136

Query Match 72.4%; Score 76; DB 10; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.0031;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18
|||:|||||:|||||
Db 1 RRRRRRTALDWSWLQTE 18

RESULT 9
US-09-847-946A-133
Sequence 133, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 133
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-133

Query Match 68.8%; Score 72; DB 10; Length 22;
Best Local Similarity 66.7%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWLQTE 18
|||:|||||:|||||
Db 5 KRRRRRTALDWSWLQTE 22

RESULT 10
US-09-847-946A-134
Sequence 134, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A

```

; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-134

```

```

Query Match      68.6%; Score 72; DB 10; Length 22;
Best Local Similarity 66.7%; Pred. No. 0.012;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 RRMKWKKTALDWSWLQTE 18
   : : : : : : : : : : : :
Db 5 KRRQRRRTALDWSWLQTE 22

```

```

RESULT 11
US-09-847-946A-143
; Sequence 143, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-143

```

```

Query Match      66.7%; Score 70; DB 10; Length 13;
Best Local Similarity 86.7%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```

```

QY 1 RRMKWKKTALDWSWL 15
   : : : : : : : : : :
Db 1 RRMKWKK--LDWSWL 13

```

```

RESULT 12
US-09-847-946A-144
; Sequence 144, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:

```

```

; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 144
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-144

```

```

Query Match      65.7%; Score 70; DB 10; Length 13;
Best Local Similarity 86.7%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```

```

QY 1 RRMKWKKTALDWSWL 15
   : : : : : : : : : :
Db 1 RRMKWKK--LDWSWL 13

```

```

RESULT 13
US-09-847-946A-137
; Sequence 137, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-137

```

```

Query Match      66.7%; Score 70; DB 10; Length 22;
Best Local Similarity 70.6%; Pred. No. 0.022;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 RRMKWKKTALDWSWLQTE 18
   : : : : : : : : : :
Db 6 RRRQRRRTALDWSWLQTE 22

```

```

RESULT 14
US-09-847-946A-138

```

Search completed: September 29, 2004, 17:08:16
Job time : 129 secs

Thu Sep 30 09:09:14 2004

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; Sequence 138, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: anti-inflammatory compound
; US-09-847-946A-138

```

```
Query Match          66.7%; Score 70; DB 10; Length 22;
Best Local Similarity 70.6%; Pred. No. 0.022;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

2 RNKWKKTALDWSWLOQTE 18
| : ::||| ||||
6 RQOARRTALDWSWLOQTE 22

DBD

RESULT 15
US-09-847-946A-139
; Sequence 139, Application US/09847946A
; Publication No. US20030054959A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847_946A

```
Query Match      64.8%; Score 68; DB 10; Length 22;
Best Local Similarity 84.6%;
Pred. No. 0.04;
Matches 11: Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 KKTALDWSWLQTE 18
      ::|||
Db     10 RRTALDWSWLQTE 22
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 16:49:34 ; Search time 39 Seconds
(without alignments)
44.396 Million cell updates/sec

Title: US-09-847-946B-131

Perfect score: 105

Sequence: 1 RRMKWKKTALDWSWLQTE 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	52.5	50.0	354	2 F97882	hypothetical prote
2	52.5	50.0	354	2 C95011	conserved domain p
3	49	46.7	588	2 AF2542	hypothetical prote
4	48	45.7	251	2 E70521	probable phosphor
5	48	45.7	549	2 A87347	hypothetical prote
6	48	45.7	643	2 B69184	hypothetical prote
7	47	44.8	1018	2 JC4375	DNA-directed DNA p
8	46	43.8	117	2 TL1933	NADH2 dehydrogenas
9	46	43.8	233	2 B96652	protein F23N19.5 [
10	46	43.8	408	2 S75900	hypothetical prote
11	46	43.8	552	2 A70709	probable pIRBa pro
12	46	43.8	1001	2 C98779	protein T203.9 [i
13	46	43.8	1038	2 T25033	hypothetical prote
14	45.5	43.3	791	2 AC0017	conserved hypotet
15	45	42.9	109	2 S60468	NADH2 dehydrogenas
16	45	42.9	118	2 S25944	NADH2 dehydrogenas
17	45	42.9	118	2 T64028	hypothetical prote
18	45	42.9	122	2 S78167	NADH2 dehydrogenas
19	45	42.9	126	2 E70430	NADH2 dehydrogenas
20	45	42.9	132	2 E97760	NADH2 dehydrogenas
21	45	42.9	207	2 D70589	probable cobA prot
22	44.5	42.4	871	2 G84601	probable protein k
23	44.5	42.4	878	2 T08559	protein kinase hom
24	44	41.9	105	2 A27471	homeotic protein R
25	44	41.9	119	2 A03314	homeotic protein m
26	44	41.9	229	2 A28329	homeotic protein H
27	44	41.9	258	2 JC6307	homeobox protein B
28	44	41.9	344	2 T34470	homeobox protein c
29	44	41.9	380	2 T42755	tyrosylprotein sul

30	43.5	41.4	253	2 T16918	hypothetical prote
31	43.5	41.4	460	2 I40799	endo-1,4-beta-gluc
32	43	41.0	75	2 I51341	homeo box protein
33	43	41.0	135	2 D82705	hypothetical prote
34	43	41.0	136	2 G64701	hypothetical prote
35	43	41.0	217	2 T43082	transfer complex p
36	43	41.0	231	2 S29096	2-haloacid halidon
37	43	41.0	353	2 A87469	ubiquinol oxidase
38	43	41.0	516	2 T10000	cytochrome P450 (C
39	43	41.0	524	2 T09944	probable cytochrom
40	43	41.0	805	2 T49385	hypothetical prote
41	42.5	40.5	209	2 B4452	translation initia
42	42.5	40.5	251	2 S03211	hypothetical prote
43	42.5	40.5	426	2 AH2144	hypothetical prote
44	42.5	40.5	545	2 T00485	probable phosphori
45	42.5	40.5	740	1 B65136	yhgF protein - Esc

ALIGNMENTS

RESULT 1

F97882

hypothetical protein spr0086 [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C:Accession: F97882

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.

A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: F97882

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-354 <KUR>

A:Cross-references: GB:AE007317; PIDN:AAK98890.1; PID:gl5457621; GSPDB:GN00174

C:Genetics:

A:Gene: spr0086

Query Match 50.0%; Score 52.5; DB 2; Length 354;

Best Local Similarity 66.7%; Pred.No.1.9;

Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 2 RRMKWKKTALD-WSWL 15

Db 141 RDKWKEQVLDWFWL 155

||||: ||| |||

||||: ||| |||

RESULT 2

C95011

conserved domain protein SP0097 [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C:Accession: C95011

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.;

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison

A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: C95011

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-354 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK74284.1; PID:gl4971563; GSPDB:GN00164; TIGR:SP

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP0097

Query Match 50.0%; Score 52.5; DB 2; Length 354;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 RMKWKKTALD-WSWL 15
 |||: |||: |||:
 Db 141 RDKWKEQVLDWFWSL 155

RESULT 3
 AF2542
 hypothetical protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AF2542
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AF2542
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-588 <KUR>
 A:Cross-references: GB:AP003602; PIDN:BAB77268.1; PID:gl7134710; GSPDB:GN00181
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all7625
 A:Genome: plasmid

Query Match 46.7%; Score 49; DB 2; Length 588;
 Best Local Similarity 54.5%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 WKTALDWSWL 15
 ||: |||: |||:
 Db 40 WKQEGLDGWV 50

RESULT 4
 E70521
 probable phosphotransferase - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: E70521
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: E70521
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-251 <COL>
 A:Cross-references: GB:Z97188; GB:AL123456; NID:g3261805; PIDN:CAB10016.1; PID:g2224828
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3817
 C:Superfamily: kanamycin kinase

Query Match 45.7%; Score 48; DB 2; Length 251;
 Best Local Similarity 30.0%; Pred. No. 6.4;
 Matches 9; Conservative 4; Mismatches 5; Indels 12; Gaps 1;

QY 1 RMKWKKTALD-----DWSWLQTE 18
 |||: |||: |||: |||: |||:
 Db 64 RRURWAAPYLAVPRVLGVGDGWLHTD 93

RESULT 5

A87347
 hypothetical protein CC0788 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: A87347
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koloski, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87347
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-549 <STO>
 A:Cross-references: GB:AE005673; NID:gl3422029; PIDN:AAK22773.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0788

Query Match 45.7%; Score 48; DB 2; Length 549;
 Best Local Similarity 53.8%; Pred. No. 15;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KWKKTALDWSWLQ 16
 ||: |||: |||:
 Db 447 KWQFGASDWTWLK 459

RESULT 6
 B69184
 hypothetical protein MTH632 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
 C:Accession: B69184
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: B69184
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-643 <MTH>
 A:Cross-references: GB:AE000844; GB:AE000666; NID:g2621707; PIDN:AAB85138.1; PID:g26217
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH632
 C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH632

Query Match 45.7%; Score 48; DB 2; Length 643;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RMKWKKTALDWSW 14
 |||: |||: |||:
 Db 187 RLSWERTAEDEFIW 200

RESULT 7
 JC4375
 DNA-directed DNA polymerase (EC 2.7.7.7) gamma, mitochondrial - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: DNA polymerase gamma
 C:Species: Schizosaccharomyces pombe
 C:Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 17-Mar-1999
 C:Accession: JC4375; S57641
 R:Ropp, P.A.; Copeland, W.C.
 Gene 165, 103-107, 1995
 A:Title: Characterization of a new DNA polymerase from Schizosaccharomyces pombe: A protein
 A:Reference number: JC4375; MUID:96084961; PMID:7489897
 A:Accession: JC4375
 A:Molecule type: DNA
 A:Residues: 1-1018 <ROP>

A;Cross-references: EMBL:Z47976
C;Comment: This enzyme is unique among the eukaryotic DNA polymerase, and is the only DN
C;Genetics:
A;Gene: pol gamma
A;Map position: III
C;Superfamily: DNA-directed DNA polymerase gamma chain
C;Keywords: DNA replication; mitochondrion; nucleotidyltransferase
F;169-179/Region: exonuclease pattern A
F;223-230/Region: exonuclease pattern B
F;351-355/Region: exonuclease pattern C

Query Match 44.8%; Score 47; DB 2; Length 1018;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RMKWKKTALDWS 13
Db 495 RLKWKXPLAWS 506
|:|||||

RESULT 8
T11933
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Prototheca wickerhamii mitochond
C;Species: mitochondrion Prototheca wickerhamii
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C;Accession: T11933
R;Wolff, G.; Plante, I.; Lang, B.F.; Kueck, U.; Burger, G.
J. Mol. Biol. 237, 75-86, 1994
A;Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca w
A;Reference number: Z17373; MUID:94180393; PMID:8133522
A;Accession: T11933
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-117 <WOL>
A;Cross-references: EMBL:U02970; NID:9467843; PID:9467865; PIDN:AAID12652.1
A;Experimental source: strain 263-11
C;Genetics:
A;Genome: mitochondrion
A;Note: nad3
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 43.8%; Score 46; DB 2; Length 117;
Best Local Similarity 70.0%; Pred. No. 5.7; Indels 1; Mismatches 2; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KWKKTALDWS 13
Db 108 EMKKGALDWS 117
|:|||||

RESULT 9
B96652
protein F23N19.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96652
R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: AB6141; MUID:21016719; PMID:11130712
A;Accession: B96652
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <STO>
A;Cross-references: GB:AE005173; NID:96630448; PIDN:AAF19536.1; GSPDB:GN00141

C;Genetics:

A;Gene: F23N19.5
A;Map position: 1

Query Match 43.8%; Score 46; DB 2; Length 233;
Best Local Similarity 38.9%; Pred. No. 12;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 RMKWKKTALDWSLQTE 18
Db 61 RQVRWSKPSLWCKLNTD 78
|:|||||

RESULT 10

S75900

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S75900

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

s.
A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S75900

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-408 <KAN>

A;Cross-references: EMBL:D90913; GB:AB001339; NID:91653348; PIDN:BAA18359.1; PID:dl0190

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Start codon: GTG

Query Match 43.8%; Score 46; DB 2; Length 408;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 WKTALDWSW 14
Db 62 WGKTAESWSW 71
|:|||||

RESULT 11

A70709

probable ptrBa protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C;Accession: A70709

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: A70709

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-552 <COL>

A;Cross-references: GB:Z80236; GB:AL123456; NID:g3261638; PIDN:CAB02372.1; PID:e266572;

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: ptrBa

Query Match 43.8%; Score 46; DB 2; Length 552;
Best Local Similarity 46.7%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RMKWKKTALDWSWL 15
Db 515 RYERWKETAFOYQWGL 529
|:|||||

RESULT 12

C88779
 protein T20D3.9 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: C88779
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
 A:Reference number: A15000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 35, 1999
 A:Accession: C88779
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1001 <STO>
 A:Cross-references: GB:chr_IV; PIDN:CAA92492.1; PID:G3879943; GSPDB:GNC00022; CESP:T20D3.9
 C:Genetics:
 A:Gene: T20D3.9
 A:Map position: 4
 C:Superfamily: Caenorhabditis elegans hypothetical protein T20D3.9

Query Match 43.8%; Score 46; DB 2; Length 1001;
 Best Local Similarity 54.5%; Pred. No. 55;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTALDWSMLOT 17

Db 548 RTALDWTWTD 558
 :||:|||||

RESULT 13

T25033
 hypothetical protein T20D3.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T25033
 R:Lloyd, C.
 submitted to the EMBL Data Library, December 1995
 A:Reference number: Z19971
 A:Accession: T25033
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1038 <WIL>
 A:Cross-references: EMBL:Z68220; PIDN:CAA92492.2; GSPDB:GNC00022; CESP:T20D3.9
 A:Experimental source: clone T20D3
 C:Genetics:
 A:Gene: CESP:T20D3.9
 A:Map position: 4
 A:Introns: 36/3; 341/3; 380/1; 574/2; 771/2; 966/1; 1010/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein T20D3.9

Query Match 43.8%; Score 46; DB 2; Length 1038;
 Best Local Similarity 54.5%; Pred. No. 57;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTALDWSMLOT 17

Db 585 RTALDWTWTD 595
 :||:|||||

RESULT 14

AC0017
 conserved hypothetical protein YP00134 [imported] - Yersinia pestis (strain C092)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AC0017
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AC0017
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-791 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC88997.1; PID:G15978239; GSPDB:GN00175
 C:Genetics:
 A:Gene: YP00134
 C:Superfamily: hypothetical protein ydcI

Query Match 43.3%; Score 45.5; DB 2; Length 791;
 Best Local Similarity 33.3%; Pred. No. 51;
 Matches 7; Conservative 5; Mismatches 2; Indels 7; Gaps 1;

QY 5 WKKTALDWSW-----LQTE 18

Db 273 WRKAVVNTWRIKVLHLETE 293
 :||:|||||

RESULT 15

S60466
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Scotch pine mitochondrion (fragment)
 C:Species: mitochondrion Pinus sylvestris (Scotch pine)
 C>Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 03-Jun-2002
 C:Accession: S60466; S60467; S54120
 R:Karpinska, B.; Karpinski, S.; Haebergren, J.E.
 Curr. Genet. 28, 423-428, 1995
 A:Title: The genes encoding subunit 3 of NADH dehydrogenase and ribosomal protein S12
 A:Reference number: S60467; MUID:96155621; PMID:8575014
 A:Accession: S60468
 A:Molecule type: mRNA
 A:Residues: 1-109 <KAR>
 A:Cross-references: EMBL:X86217
 A:Note: 6-Leu, 18-Leu, 21-Ser, 33-Tyr, 37-Phe, 40-Phe, 53-Leu, 55-Ser, 57-Leu, 61-Phe, Ttp are due to RNA editing
 A:Accession: S60467
 A:Molecule type: DNA
 A:Residues: 1-5, 'S', 7-17, 'P', 19-20, 'P', 22-32, 'H', 34-36, 'S', 38-39, 'S', 41-52, 'P', 54, 'P', 55, 'S', 107, 'R', 109 <KAW>
 A:Cross-references: EMBL:X86217
 C:Genetics:
 A:Gene: nad3
 A:Genome: nad3
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 3
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 42.9%; Score 45; DB 2; Length 109;
 Best Local Similarity 77.8%; Pred. No. 7.5;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KWKTALD 12

Db 100 EWKKGALDW 108
 :||:|||||

Search completed: September 29, 2004, 16:57:03
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 16:41:10 ; Search time 23 Seconds
(without alignments)
40.751 Million cell updates/sec

Title: US-09-847-946B-131

Perfect score: 105
Sequence: 1 RRMKKKALDWSWLQTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	61.0	756	1 IKKB HUMAN	O14920 homo sapien
2	54	51.4	757	1 IKKB MOUSE	O88351 mus musculus
3	54	51.4	757	1 IKKB RAT	O9qy78 rattus norv
4	48	45.7	313	1 IRF1_CHICK	O90876 gallus gall
5	47	44.8	207	1 BRX1_CHICK	O9w6d8 gallus gall
6	47	44.8	225	1 BRX1 HUMAN	O9hbul homo sapien
7	47	44.8	225	1 BRXB CHICK	O9ded6 gallus gall
8	47	44.8	254	1 BRX1 MOUSE	O9ex42 mus musculus
9	47	44.8	1018	1 DPOG SCHPO	O12704 schizosacch
10	46	43.8	117	1 NU3M PROWI	O37625 protheteca
11	45	42.9	118	1 NU3M MARPO	P26847 marchantia
12	45	42.9	118	1 NU3M PINSY	O36664 pinus sylve
13	45	42.9	118	1 YE16 HABIN	P44188 haemophilus
14	45	42.9	122	1 NU3M RECAM	O21273 reclinomona
15	45	42.9	123	1 NUOA RICCN	O92id5 rickettsia
16	45	42.9	2003	1 NTC4 HUMAN	O99466 homo sapien
17	44	41.9	105	1 HXA7 RAT	P09634 rattus norv
18	44	41.9	133	1 BRX2 SHEEP	O9n0m2 ovis aries
19	44	41.9	228	1 BRX2 MOUSE	O08686 mus musculus
20	44	41.9	229	1 HXA7 HUMAN	P02830 mus musculus
21	44	41.9	254	1 BRX2 HUMAN	O9umc3 homo sapien
22	44	41.9	344	1 HM10 CAEEL	P41935 caenorhabdi
23	44	41.9	380	1 TP08 CAEEL	O77081 mycothecia
24	44	41.9	1390	1 RPOB MYCGA	P47715 mycoplasma
25	43.5	41.4	460	1 GUN2 CLOJO	P37701 clostridium
26	43.5	41.4	762	1 YHGF HABIN	P71353 haemophilus
27	43	41.0	75	1 HWSA SALSA	P09636 salmo salar
28	43	41.0	230	1 HADA BURCE	O51645 burkholderi
29	43	41.0	524	1 CP72 CATRO	O05047 catharanthu
30	42.5	40.5	209	1 IFE2 WHEAT	O03389 triticum ae
31	42.5	40.5	251	1 Y29K SSV1	P20202 sulfolobus
32	42.5	40.5	773	1 YHGF ECOLI	P46837 escherichia
33	42	40.0	117	1 NU3M_LUMTE	O34950 lumbricus t

RESULT 1

IKKB HUMAN

ID IKKB HUMAN STANDARD; PRT; 756 AA.

AC O14920; O75327; 118 40.0 118 1 NU3M ALLCE

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)

DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase

DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).

GN IKKB OR IKKB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.

RC TISSUE=Cervical carcinoma;

RX MEDLINE=98008813; PubMed=9346484;

RA Li J.W., Young D.B., Murray B.W., Shevchenko A., Bennett B.L.,

RA Mercutio F., Zhu H., Murray B.W., Mann M., Manning A., Rao A.;

RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for

RT NF-kappaB activation.";

RT Science 278:860-866(1997).

RL [2]

RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.

RX MEDLINE=98008814; PubMed=9346485;

RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;

RA "IkappaB kinase-beta: NF-kappaB activation and complex formation with

RT IkappaB kinase-alpha and NIK.";

RL Science 278:866-869(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=99032998; PubMed=9813230;

RA Hu M.C.-T., Wang Y.-P.;

RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and

embryonic tissues but localized to different human chromosomes.";

RL Gene 222:31-40(1998).

RN [4]

RP SEQUENCE FROM N.A., AND GENE MAPPING.

RX MEDLINE=98438415; PubMed=9763654;

RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;

RA "Assignment of IkappaB kinase beta (IKKB) to human chromosome band

8p12-->p11 by in situ hybridization.";

RT Cytogenet. Cell Genet. 82:32-33(1998).

RN [5]

RP SEQUENCE OF 1-256 FROM N.A.

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gurnatne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP IKK PHOSPHORYLATION
RX MEDLINE=99038238; PubMed=9819420;
RY Nemoto S., DiDonato J.A., Lin A.;
RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343 (1998).
RN [7]
RP REVIEW
RX MEDLINE=20178139; PubMed=10712233;
RY Jobin C., Sartor R.B.;
RA "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection.";
RL Am. J. Physiol. 278:C451-C462 (2000).
RN [8]
RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA3; IKKA AND IKKBK.
RX MEDLINE=21968797; PubMed=11971985;
RY Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA O'Malley B.W.;
RA "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT activity by I kappa B kinase.";
RL Mol. Cell. Biol. 22:3549-3561 (2002).
CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3 (By similarity).
CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBK
CC and CREBBP
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC peripheral blood.
CC -!- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPAB KINASE SUBFAMILY.
CC
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CC
CC -----
CC EMBL; AF029684; AAC51860.1; -
CC DR EMBL; AF080158; AAD08997.1; -
CC DR EMBL; AF034416; AAC64675.1; -
CC DR EMBL; BC006231; AAH06231.1; -
CC DR HSSP; Q63450; 1A06.
CC DR Genew; HGNC:5960; IKKBK.
CC DR MIM; 603258; -
CC DR GO; GO:0005737; Cytoplasm; NAS.
CC DR GO; GO:0005524; F-ATP binding; NAS.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0016563; F:transcriptional activator activity; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00240; ubiquitin; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT NP_BIND 21 29 NEMO-BINDING.
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 ATP (BY SIMILARITY).
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MUTAGEN 181 181 K->A: LOSS OF KINASE ACTIVITY AND NO
FT MUTAGEN 44 44 EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 177 177 S->B: FULL ACTIVATION.
FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 181 181 S->B: FULL ACTIVATION.
FT CONFLICT 231 255 WHSKVRQKSDVIVSDELNGTVKF -> CVRWMPGTVAHS
FT CONFLICT 425 425 CNPSTVLGGGRWI (IN REF. 5).
FT CONFLICT 425 425 Q -> H (IN REF. 1).
SQ SEQUENCE 756 AA; 86563 MW; F9CADF671AE9E14E CRC64;
Query Match 61.0%; Score 64; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TALDWSWLQTE 18
Db 735 TALDWSWLQTE 745
RESULT 2
IKKB MOUSE
ID IKKB_MOUSE STANDARD; PRT; 757 AA.
AC 088351; Q9RUJ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.
RX STRAIN=C57BL/6; TISSUE=Spleen;
RC MEDLINE=98188238; PubMed=9520401;
RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of Ikb.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

[3] DEVELOPMENTAL STAGE.
 MEDLINE=9455228; PubMed=10523828;
 Hu M.C.-T., Wang Y.-P., Qiu W.R., Tan T.-H.;
 "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 developmentally regulated protein kinase.";
 Oncogene 18:5514-5524(1999).
 [4]
 IKK PHOSPHORYLATION.
 MEDLINE=99038238; PubMed=9819420;
 Nemoto S., DiDonato J.A., Lin A.;
 "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 Mol. Cell. Biol. 18:7336-7343(1998).
 [5]
 REVIEW.
 MEDLINE=20178139; PubMed=10712233;
 Jobin C., Sartor R.B.;
 "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 Am. J. Physiol. 278:C451-C462(2000).
 -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 Heterodimers form the active complex. The tripartite complex can
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50
 complex. Phosphorylated IKK-alpha is further released from the
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 and CREBBP (By similarity).
 -!- SUBCELLULAR LOCATION: Cytoplasmic.
 -!- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
 -!- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
 the mouse embryo, at E9.5 day its expression begins to be
 localized to the brain, neural ganglia, neural tube, and in liver
 at E12.5 day. At E15.5 day, the expression is further restricted
 to specific tissues of the embryo.
 -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 Weakly autophosphorylated.
 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 IKAPPAB KINASE SUBFAMILY.

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 EMBL; AF026524; AAC23557.1; -;
 EMBL; AF089810; AAD52095.1; -;
 HSSP; Q63450; 1A06.
 MGD; MGI:1338071; Ikbb.
 InterPro; IPR000719; Prot kinase.
 InterPro; IPR008271; Ser thr pkin AS.
 InterPro; IPR001245; Tyr_pkinase.
 Pfam; PF00699; pkinase; 1.
 PRINTS; PR00109; TYRKINASE.
 ProDom; PD000001; Prot kinase; 1.
 PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 PROSITE; PS00108; PROTEIN KINASE ST; 1.
 PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 Transferase; Serine/threonine-protein kinase; ATP-binding;
 Phosphorylation.
 DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT

FT ACT SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 K -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 736 TLDWSLQMEDEERCSLEQACD -> VTA (IN REF. 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;
 Query Match 51.4%; Score 54; DB 1; Length 757;
 Best Local Similarity 81.8%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 8 TALDWSLQTE 18
 Db 735 TLDWSLQME 745
 RESULT 3
 IKKB_RAT STANDARD; PRT; 757 AA.
 ID IKKB_RAT
 AC Q9QY78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB).
 DE IKKB OR IKKB.
 OS Rattus norvegicus (Rat).
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Sun S., Ravid K.;
 RT "IKK beta in megakaryocyte differentiation.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 Am. J. Physiol. 278:C451-C462(2000).
 CC -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
 the dissociation of the inhibitor/NF-kappa-B complex and
 ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3.
 CC -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.
 CC Heterodimers form the active complex. The tripartite complex can
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50
 CC complex. Phosphorylated IKK-alpha is further released from the
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
 CC and CREBBP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 CC Weakly autophosphorylated.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF115282; AAP21978.1; -.
CC HSP; Q63450; IAO6
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation.
CC FT DOMAIN 15 300 PROTEIN KINASE.
CC FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
CC FT NP_BIND 737 742 NEMO-BINDING.
CC FT BINDING 21 29 ATP (BY SIMILARITY).
CC FT ACT_SITE 44 44 ATP (BY SIMILARITY).
CC FT MOD_RES 145 145 BY SIMILARITY.
CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
CC SQ SEQUENCE 757 AA; 86866 MW; 3AFPE46A7DF91F9C CRC64;

Query Match 51.4%; Score 54; DB 1; Length 757;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TALDWSWLOTE 18
DB 735 TTLDWSWLOME 745

RESULT 4
IRF1_CHICK STANDARD; PRT; 313 AA.
AC Q90876;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interferon regulatory factor 1 (IRF-1).
GN IRF1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95241453; PubMed=7536924;
RA Jungwirth C., Rebber M., Ozato K., Degen H.J., Schultz U.,
RA David I.B.;
RT "Chicken interferon consensus sequence-binding protein (ICSBP) and
RT interferon regulatory factor (IRF) 1 genes reveal evolutionary
RT conservation in the IRF gene family."
RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).
CC -!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF
CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
CC CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the IRF family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L39766; AAA62160.1; -.
CC HSP; P15314; IIF1.
CC TRANSFAC; T05092; -.
CC InterPro; IPR001346; IRF.
CC Pfam; PF00605; IRF; 1.
CC PRINTS; PR00267; INTERFERGFCF.
CC ProDom; PD002355; IRF; 1.
CC SMART; SM00348; IRF; 1.
CC PROSITE; PS00601; IRF; 1.
CC Transcription regulation; DNA-binding; Activator; Nuclear protein.
CC DNA_BIND 7 109 TRYPTOPHAN PENTAD REPEAT.
CC SQ SEQUENCE 313 AA; 36009 MW; 0895FA3736FA7463 CRC64;

Query Match 45.7%; Score 48; DB 1; Length 313;
Best Local Similarity 56.2%; Pred. No. 5.8;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 RMKKKKTALDWSWLOT 17
DB 287 RMWDQKSLQFSWLDLT 302

RESULT 5
BRX1_CHICK STANDARD; PRT; 207 AA.
AC Q9W6D8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein Barx-like 1 (Fragment).
GN BARX1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99228399; PubMed=10213385;
RA Barlow A.J., Bogardi J.P., Ladherr R., Francis-West P.H.;
RT "Expression of chick Barx-1 and its differential regulation by FGF-8
RT and BMP signaling in the maxillary primordia."
RL Dev. Dyn. 214:291-302(1999).
CC -!- FUNCTION: Transcription factor, which may be involved in
CC craniofacial development, in odontogenesis and in stomach
CC organogenesis. May have a role in the differentiation of molars
CC from incisors. Binds to a regulatory module of the NCAM promoter.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Expressed predominantly in the facial
CC primordia, developing stomach, and proximal limbs.
CC -!- DEVELOPMENTAL STAGE: First detectable in the facial primordia at
CC stage 18 after neural crest migration. Expressed in regions
CC derived from both mid- and hindbrain neural crest. Also expressed
CC in the developing cartilage elements of the limb, first within a
CC restricted population in the prechondrogenic mesenchyme and later
CC in the rounded chondrocytes at the epiphyses of developing long
CC bones.
CC -!- SIMILARITY: Belongs to the BAR homeobox family.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC -----
CC EMBL; AF116460; AAD21043.1; -.
CC DR HSP; P14653; 1B72.
CC DR GO; GO:0000228; C:nuclear chromosome; NAS.
CC DR TRANSFAC; T03934; -.
CC DR InterPro; IPR001356; Homeobox.
CC DR InterPro; IPR000047; HTH_lambrepresr.
CC DR Pfam; PF00046; homeobox; 1.
CC DR PRINTS; PR00024; HOMEBOX.
CC DR PRINTS; PR00031; HTHREPRESSR.
CC DR ProDom; PD000010; Homeobox; 1.
CC DR SMART; SM00389; HOX; 1.
CC DR PROSITE; PS00027; HOMEBOX 1; 1.
CC DR PROSITE; PS00071; HOMEBOX 2; 1.
CC KW Homeobox; Transcription regulation; DNA-binding; Nuclear protein.
CC FT NON_TPR 1 1
CC FT DNA_BIND 95 154 HOMEBOX.
CC FT SEQUENCE 207 AA; 22467 MW; 3EDE64A91D3BCE84 CRC64;
CC
CC Query Match 44.8%; Score 47; DB 1; Length 207;
CC Best Local Similarity 52.9%; Pred. No. 5.3;
CC Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
CC
CC QY 1 RRMKWKKTALDMSWLQT 17
CC Db ||||||| |:::
CC 146 RRMKWKKIVLQGGGLES 162
CC
CC RESULT 6
CC BRXL_HUMAN STANDARD; PRT; 225 AA.
CC ID BRXL_HUMAN
CC AC Q9HBU1;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Homeobox protein BarH-like 1.
CC GN BARX1.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A., AND VARIANT ALA-19.
CC RC TISSUE=Craniofacial;
CC RX MEDLINE=20453194; PubMed=10995576;
CC RA Gould D.B., Walter M.A.;
CC RT "Cloning, characterization, localization, and mutational screening of
CC RT the human BARX1 gene.";
CC RL Genomics 68:336-342(2000).
CC CC -!- FUNCTION: Transcription factor, which may be involved in
CC CC craniofacial development, in ontogenesis and in stomach
CC CC organogenesis. May have a role in the differentiation of molars
CC CC from incisors. Binds to a regulatory module of the NCAM promoter.
CC CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC CC -!- TISSUE SPECIFICITY: Widely expressed. Expressed at higher levels
CC CC in testis and heart. Detected in craniofacial tissue and adult
CC CC iris, but not in lymphocytes, fibroblasts, choroid retina, retinal
CC CC pigment epithelium, kidney, or fetal liver.
CC CC -!- POLYMORPHISM: The polymorphism is not associated with Axenfeld-
CC CC Reiger syndrome (ARS), iridogoniodysgenesis syndrome (IGDS) or
CC CC related ocular malformations.
CC CC -!- SIMILARITY: Belongs to the BAR homeobox family.
CC CC -!- SIMILARITY: Contains 1 homeobox domain.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC EMBL; AF213356; AAG23738.1; -.
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DR HSP; P14653; 1B72.
DR Genew; HGNC:955; BARX1.
DR MIM; 603260; -.
DR GO; GO:0000228; C:nuclear chromosome; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0007275; P:development; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
DR KW Homeobox; Transcription regulation; DNA-binding; Nuclear protein;
KW Polymorphism.
KW DNA_BIND 113 172 HOMEBOX.
FT DOMAIN 15 24 POLY-ALA.
FT VARIANT 19 19 T->A.
FT SEQUENCE 225 AA; 24061 MW; A7907BB4668F3393 CRC64;
CC
CC Query Match 44.8%; Score 47; DB 1; Length 225;
CC Best Local Similarity 52.9%; Pred. No. 5.7;
CC Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
CC
CC QY 1 RRMKWKKTALDMSWLQT 17
CC Db ||||||| |:::
CC 164 RRMKWKKIVLQGGGLES 180
CC
CC RESULT 7
CC BRXB_CHICK STANDARD; PRT; 247 AA.
CC ID BRXB_CHICK
CC AC Q9DED6;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Homeobox protein BarH-like 1b (Bar class homeoprotein BarXlb).
CC GN BARX1B.
CC OS Gallus gallus (Chicken).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC OC Gallus.
CC OX NCBI_TaxID=9031;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=21259836; PubMed=11359793;
CC RA Nakamura M., Nishida W., Mori S., Hiwada K., Hayaashi K., Sobue K.;
CC RT "Transcriptional activation of beta-tropomyosin mediated by serum
CC RT response factor and a novel BarX homologue, BarXlb, in smooth muscle
CC RT cells.";
CC RL J. Biol. Chem. 276:18313-18320(2001).
CC CC -!- FUNCTION: Transcription factor which is involved with the serum
CC CC response factor (SRF) in the smooth muscle cell-specific
CC CC transcription of the beta-tropomyosin gene in the upper digestive
CC CC organs and their attached arteries.
CC CC -!- SUBUNIT: Interacts with serum response factor (SRF).
CC CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC CC -!- TISSUE SPECIFICITY: Expressed in smooth muscle cells of the upper
CC CC digestive organs and their attached arteries and to craniofacial
CC CC structures.
CC CC -!- SIMILARITY: Belongs to the BAR homeobox family.
CC CC -!- SIMILARITY: Contains 1 homeobox domain.
CC CC -----
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CC EMBL; AF213356; AAG23738.1; -.
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CC -----
CC EMBL; AB044371; BAB18919.1; -.
CC HSSP; P14653; 1B72.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR000047; HTH_lambdarepressr.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; Transcription regulation; DNA-binding; Nuclear protein.
KW DNA_BIND 135 194 HOMEBOX.
FT SEQUENCE 247 AA; 27027 MW; A72EFA192F8624F CRC64;
SQ -----
Query Match 44.8%; Score 47; DB 1; Length 247;
Best Local Similarity 52.9%; Pred. No. 6.3;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 RRMKWKKTALDWSWLTQ 17
Db 186 RRMKWKKTALDWSWLTQ 202
RESULT 8
ID BRX1 MOUSE STANDARD; PRT; 254 AA.
AC Q9ER42; O09066; P70159; Q9ERV2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-WAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein BarH-like 1.
GN BARX1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=Head;
RC TISSUE=Head;
RA Buchner G.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 30-254 FROM N.A.
RC STRAIN=BALE/c;
RA Meech R., Edelman D.B., Jones F.S.;
RT "Characterization of the mouse Barx1 gene.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 108-254 FROM N.A.
RC STRAIN=NMRI;
RA Tissier-Seta J.P., Mucchielli M.L., Mark M., Mattei M.-G., Goridis C.,
RT Brunet J.F.;
RT "Barx1, a new mouse homeodomain transcription factor expressed in
RT cranio-facial ectomesenchyme and the stomach.";
RL Mech. Dev. 51:3-15(1995).
CC -1- FUNCTION: Transcription factor, which may be involved in
CC craniofacial development, in odontogenesis and in stomach
CC organogenesis. May have a role in the differentiation of molars
CC from incisors. Binds to a regulatory module of the NCAM promoter.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- TISSUE SPECIFICITY: Expressed predominantly in the facial
CC primordia, developing stomach, and proximal limbs.
CC -1- DEVELOPMENTAL STAGE: Expressed in areas of the first and second
CC branchial arches, before any apparent cellular or morphologic
CC differentiation. Later in development, all expressing tissue in
CC this region, including the mesenchyme underlying the olfactory
CC epithelium, the primary and secondary palate, the molar tooth
CC papillae, and the stroma of the submandibular gland, appear to be
CC derived from ectomesenchyme of neural crest origin. By day 16.5,

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CC all areas except the developing molars are BARX1-negative. In
CC addition, BARX1 marks the area of the future stomach in the
CC primitive gut at embryonic day 9.5, and is present in the
CC mesenchymal wall of the stomach until embryonic day 16.5.
CC -1- SIMILARITY: Belongs to the BAR homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-30 is the initiator.
CC -----
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CC -----
CC EMBL; AJ297677; CAC10357.1; -.
CC EMBL; AF277160; AAG18573.1; -.
CC EMBL; Y07960; CAA6257.1; -.
CC HSSP; P14653; 1B72.
CC TRANSFAC; T02403; -.
CC MGD; MGI:103124; Barx1.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR000047; HTH_lambdarepressr.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESSR.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; Transcription regulation; DNA-binding; Nuclear protein.
KW DNA_BIND 142 201 HOMEBOX.
FT DOMAIN 44 53 POLY-ALA.
FT DOMAIN 254 AA; 27282 MW; 48586B28F4A23FCC CRC64;
SQ SEQUENCE 254 AA; 44.8%; Score 47; DB 1; Length 254;
Query Match 52.9%; Pred. No. 6.5;
Best Local Similarity 52.9%; Pred. No. 6.5;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 RRMKWKKTALDWSWLTQ 17
Db 193 RRMKWKKTALDWSWLTQ 209
RESULT 9
ID DPOG SCHPO STANDARD; PRT; 1018 AA.
AC Q12704; Q96WV3; Q9P714;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase gamma (BC 2.7.7.7) (Mitochondrial DNA polymerase
DE catalytic subunit).
GN MIPI OR SPC24B10.22 OR SPCPB16A4.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP808;
RX MEDLINE=96084961; PubMed=7489897;
RT Ropp P.A., Copeland W.C.;
RT "Characterization of a new DNA polymerase from Schizosaccharomycetes
RT pombe: a probable homologue of the Saccharomyces cerevisiae DNA
RT polymerase gamma."
RL Gene 165:103-107(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;

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RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA	Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA	Collins M., Connor A., Cronin A., Davis P., Fellwell T., Fraser A.,
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA	Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA	Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA	Woodward J., Voiclaert G., Aert R., Robben J., Gymonprez B.,
RA	Waltjens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA	Gabel C., Fuchs M., Fritz C., Holzer E., Moest D., Hilbert H.,
RA	Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
RA	Domiguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA	Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT	"The genome sequence of Schizosaccharomyces pombe.";
RL	Nature 415:871-880(2002).
CC	-I- FUNCTION: Involved in the replication of mitochondrial DNA.
CC	-I- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC	+ {DNA} (N);
CC	-I- COFACTOR: Magnesium.
CC	-I- SUBCELLULAR LOCATION: Mitochondrial.
CC	-I- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
CC	alpha, beta, gamma, delta, and epsilon which are responsible for
CC	different reactions of DNA synthesis.
CC	-I- SIMILARITY: Belongs to the DNA polymerase type-A family.
CC	-----
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CC	-----
DR	EMBL; Z47976; CRA88012.1; -;
DR	EMBL; AL157991; CAB76231.1; -;
DR	EMBL; AL591677; CAC39320.1; -;
DR	GeneDB_SPombe; SPCC24B10.22; -;
DR	GO; GO:0005654; C:nucleoplasm, ISS.
DR	GO; GO:0007049; P:cell cycle, ISS.
DR	GO; GO:0000084; P:S phase of mitotic cell cycle, ISS.
DR	InterPro; IPR001098; DNA pol.
DR	InterPro; IPR002297; DNA polG.
DR	Pfam; PF00476; DNA pol A; 1.
DR	PRINTS; PR00867; DNAPOIG.
DR	SMART; SMO0482; POLAC; 1.
DR	PROSITE; PS00447; DNA POLYMERASE A; FALSE NEG.
KW	Transferase; DNA-directed DNA polymerase; DNA replication;
KW	DNA-binding; Mitochondrion; Magnesium.
FT	CONFLICT 563 563 G -> C (IN REF. 1).
FT	CONFLICT 571 572 QR -> HA (IN REF. 1).
FT	CONFLICT 832 832 T -> Q (IN REF. 1).
SQ	SEQUENCE 1018 AA; 116045 MW; 9B114BC6FBEE63CA CRC64;
	Query Match 44.8%; Score 47; DB 1; Length 1018;
	Best Local Similarity 66.7%; Pred. No. 28;
	Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY	2 RMKKKKTALDWS 13
	!::
Db	495 RLKWKHKPLAWS 506

RESULT 10

NU3M_PROMI

NU3M_WARPO

STANDARD;

PRT;

117 AA.

AC

Q37625;

DT

30-MAY-2000 (Rel. 39, Created)

DT

30-MAY-2000 (Rel. 39, Last sequence update)

DT

30-MAY-2000 (Rel. 39, Last annotation update)

DE

NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3).

GN

NAD3

OS

Prototheca wickerhamii.

OG

Mitochondrion.

OC

Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;

OC

Chlorrellaceae; Prototheca.

OX

NCBI_TaxID=3111;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

STRAIN=263-11;

RX

MEDLINE=94180393; PubMed=8133522;

RA

Wolff G., Planete I., Lang B.F., Kueck U., Burger G.;

RT

"Complete sequence of the mitochondrial DNA of the chlorophyte alga

RT

Prototheca wickerhamii. Gene content and genome organization.";

RL

J. Mol. Biol. 237:75-86(1994).

CC

-I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

CC

-I- SIMILARITY: Belongs to the complex I subunit 3 family.

CC

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DR

EMBL; U02970; RAD12652.1; -;

DR

PIR; T11933; T11933.

DR

InterPro; IPR000440; Oxidored q4.

DR

Pfam; PF00507; oxidored q4; 1.

KW

Oxidoreductase; NAD; Ubiquinone; Mitochondrion.

SQ

SEQUENCE 117 AA; 13699 MW; D07FC592F30076CB CRC64;

Query Match 43.8%; Score 46; DB 1; Length 117;

Best Local Similarity 70.0%; Pred. No. 4.1;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY

4 KWKKTALDWS 13

!::|||

Db

108 EWRKALDWS 117

CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.
 CC -----
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 CC -----
 DR EMBL; M68929; AAC09408.1; -;
 DR PIR; S25944; S25944.
 DR InterPro; IPR000440; Oxidored q4.
 DR Pfam; PF00507; oxidored q4; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 118 AA; 13688 MW; 65CB28749ABA81B9 CRC64;

 CC Query Match 42.9%; Score 45; DB 1; Length 118;
 CC Best Local Similarity 77.8%; Pred. No. 5.7;
 CC Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 4 KWKKTALDW 12
 Db 109 EWKKGALDW 117

 CC RESULT 12
 CC NU3M_PINSY
 CC ID NU3M_PINSY STANDARD; PRT; 118 AA.
 CC AC Q36664;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3).
 CC GN NAD3.
 CC OS Pinus sylvestris (Scots pine).
 CC OC Mitochondrion.
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 CC OX NCBI_TaxID=3349;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND RNA EDITING.
 CC RC TISSUE=Cotyledon;
 CC RX MEDLINE=96155621; PubMed=8575014;
 CC RA Karpinska B., Karpinski S., Hallgren J.B.;
 CC RT "The genes encoding subunit 3 of NADH dehydrogenase and ribosomal
 CC RT protein S12 are co-transcribed and edited in Pinus sylvestris (L.)
 CC RT mitochondria";
 CC RL Curr. Genet. 28:423-428(1995).
 CC CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- RNA EDITING: Modified positions=15, 27, 30, 42, 46, 49, 62, 64,
 CC 66, 70, 72, 77, 78, 80, 83, 89, 92, 93, 102, 107, 108, 115,
 CC 117.
 CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.
 CC -----
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 CC -----
 DR EMBL; X86217; CAA60117.1; ALT_SEQ.
 DR PIR; S60468; S60468.
 DR InterPro; IPR000440; Oxidored q4.
 DR Pfam; PF00507; oxidored q4; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; RNA editing.
 SQ SEQUENCE 118 AA; 13669 MW; 25AC6B8F8F9F1F52 CRC64;

 CC Query Match 42.9%; Score 45; DB 1; Length 118;
 CC Best Local Similarity 77.8%; Pred. No. 5.7;
 CC Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 4 KWKKTALDW 12
 Db 109 EWKKGALDW 117

 CC RESULT 13
 CC YE16_HAEIN
 CC ID YE16_HAEIN STANDARD; PRT; 118 AA.
 CC AC P44188;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Hypothetical protein H11416 precursor.
 CC GN H11416.
 CC OS Haemophilus influenzae.
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 CC OC Pasteurellaceae; Haemophilus.
 CC OX NCBI_TaxID=727;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Rd / KW20 / ATCC 51907;
 CC RX MEDLINE=95350630; PubMed=7542800;
 CC RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 CC RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 CC RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 CC RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 CC RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 CC RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 CC RA Fife L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 CC RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 CC RA Venter J.C.;
 CC RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 CC RT Rd.";
 CC RL Science 269:496-512(1995).
 CC -----
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 CC -----
 DR EMBL; U32821; AAC23067.1; -;
 DR PIR; I64028; I64028.
 DR TIGR; H11416; -;
 DR InterPro; IPR006481; Holin_lambda.
 DR Pfam; PF05106; Phage_holin_3; 1.
 DR TIGRfams; TIGR01594; holin_lambda; 1.
 KW Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 118 HYPOTHETICAL PROTEIN H11416.
 SQ SEQUENCE 118 AA; 13516 MW; 96C85D469DF8E2EB CRC64;

 CC Query Match 42.9%; Score 45; DB 1; Length 118;
 CC Best Local Similarity 88.9%; Pred. No. 5.7;
 CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 9 ALDWSWLOT 17
 Db 10 ALIWSWLOT 18

 CC RESULT 14
 CC NU3M_RECAM
 CC ID NU3M_RECAM STANDARD; PRT; 122 AA.
 CC AC C21273;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3).

CC -----
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CC -----
CC EMBL; AF008611; AAL03023.1; ALT_INIT.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; oxidored_q4; 1.
KW Oxidoreductase; NAD; Quinone; Transmembrane; Complete proteome.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 58 88 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
SQ SEQUENCE 123 AA; 14242 MW; 5395664436F056AC CRC64;

Query Match 42.9%; Score 45; DB 1; Length 123;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KWKKTALDW 12
:|||||
Db 115 EWKKGALDW 123

Search completed: September 29, 2004, 16:54:19
Job time : 25 secs

GN NAD3.
OS Reclinomonas americana.
OC Mitochondrion.
CG Eukaryota; Jakobidae; Reclinomonas.
OX NCBI_TaxID=48483;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50394;
RX MEDLINE=97311393; PubMed=9168110;
RA Lang B.F., Burger G., O'Kelly C.J., Cedergren R., Golding G.B.,
RA Lemieux C., Sankoff D., Turmel M., Gray M.W.;
RT "An ancestral mitochondrial DNA resembling a eubacterial genome in
RT miniature";
RL Nature 387:493-497(1997).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.
CC -----
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CC -----
CC EMBL; AF007261; AAD11900.1; -.
DR PIR; S78167; S78167.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; oxidored_q4; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 122 AA; 14049 MW; 0E0BE35DF170A897 CRC64;

Query Match 42.9%; Score 45; DB 1; Length 122;
Best Local Similarity 77.8%; Pred. No. 5.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KWKKTALDW 12
:|||||
Db 113 EWKKGALDW 121

Search completed: September 29, 2004, 16:54:19
Job time : 25 secs

RESULT 15
NUOA_RICCN STANDARD; PRT; 123 AA.
AC Q92ID5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NADH-quinone oxidoreductase chain A (EC 1.6.99.5) (NADH dehydrogenase
I, chain A) (NDH-1, chain A).
GN NUOA OR RC0485.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
RL Science 293:2093-2098(2001).
CC -!- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain.
CC Couples the redox reaction to proton translocation (for every two
CC electrons transferred, four hydrogen ions are translocated across
CC the cytoplasmic membrane), and thus conserves the redox energy in
CC a proton gradient (By similarity).
CC -!- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 16:48:15 ; Search time 114 Seconds
(without alignments)
49.819 Million cell updates/sec

Title: US-09-847-946B-131
Perfect score: 105
Sequence: 1 RRMKWKKTALDWSWLQTE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52.5	50.0	354	16 Q97T58	Q97T58 streptococc
2	52.5	50.0	354	16 Q8CZC0	Q8CZC0 streptococc
3	52	49.5	756	6 Q85KV0	Q85KV0 bos taurus
4	50	47.6	1208	5 Q9U4W1	Q9U4W1 aedes aegypt
5	49	46.7	389	16 Q98U62	Q98U62 thizobium l
6	49	46.7	588	16 Q8ZS87	Q8ZS87 anabaena sp
7	48.5	46.2	274	5 Q9XYT7	Q9XYT7 cassiopea x
8	48	45.7	251	16 Q07806	Q07806 mycobacteri
9	48	45.7	251	16 Q7TVL6	Q7TVL6 mycobacteri
10	48	45.7	549	16 Q9AA20	Q9AA20 caulobacter
11	48	45.7	643	17 Q26729	Q26729 methanobact
12	48	45.7	706	16 Q8NMH7	Q8NMH7 corynebacte
13	48	45.7	833	16 Q7UL36	Q7UL36 rhodospirill
14	47.5	45.2	426	16 Q8F9T9	Q8F9T9 leptospira
15	47	44.8	100	4 Q96GH8	Q96GH8 homo sapien
16	47	44.8	703	16 Q8FML7	Q8FML7 corynebacte

17	47	44.8	1382	10 Q9FW98	Q9FW98 oryza sativ
18	47	44.8	1382	10 Q7XCU0	Q7XCU0 oryza sativ
19	46	43.8	117	8 Q94RE9	Q94RE9 lithobius f
20	46	43.8	117	8 Q9C402	Q9C402 lithobius f
21	46	43.8	209	16 Q7WHC9	Q7WHC9 bordetella
22	46	43.8	209	16 Q7W9D4	Q7W9D4 bordetella
23	46	43.8	209	16 Q7VYU4	Q7VYU4 bordetella
24	46	43.8	233	10 Q9S181	Q9S181 arabidopsis
25	46	43.8	408	16 P74265	P74265 synechocyst
26	46	43.8	441	2 Q9EZF9	Q9EZF9 streptococc
27	46	43.8	552	16 P71835	P71835 mycobacteri
28	46	43.8	718	16 Q8VKE4	Q8VKE4 mycobacteri
29	46	43.8	719	16 Q7U1A6	Q7U1A6 streptococc
30	46	43.8	862	2 Q9RPZ2	Q9RPZ2 streptococc
31	46	43.8	1022	2 Q91T54	Q91T54 streptococc
32	46	43.8	1038	5 C01261	C01261 caenorhabdi
33	45.5	43.3	621	16 Q8FPV4	Q8FPV4 corynebacte
34	45.5	43.3	740	16 Q7UAT1	Q7UAT1 shigella fl
35	45.5	43.3	773	16 Q83PW5	Q83PW5 shigella fl
36	45.5	43.3	791	16 Q8ZJH3	Q8ZJH3 versinia pe
37	45.5	43.3	849	16 Q88PJ0	Q88PJ0 pseudomonas
38	45	42.9	63	8 Q7YF66	Q7YF66 podocarpus
39	45	42.9	63	8 Q7YF59	Q7YF59 retrophyllu
40	45	42.9	66	8 Q7YF57	Q7YF57 araucaria n
41	45	42.9	116	2 Q847T5	Q847T5 aster yello
42	45	42.9	116	8 Q8M1D1	Q8M1D1 chaetospheae
43	45	42.9	118	8 Q9TC97	Q9TC97 nephroselimi
44	45	42.9	118	8 Q7YAM8	Q7YAM8 chara vulga
45	45	42.9	119	16 Q7WCT9	Q7WCT9 bordetella

ALIGNMENTS

RESULT 1

Q97T58	PRELIMINARY;	PRT;	354 AA.
ID	Q97T58		
AC	Q97T58		
DT	01-OCT-2001 (T-EMBLrel. 18, Created)		
DT	01-OCT-2001 (T-EMBLrel. 18, Last sequence update)		
DT	01-JUN-2003 (T-EMBLrel. 24, Last annotation update)		
DE	Conserved domain protein.		
GN	SP0097.		
OS	Streptococcus pneumoniae.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_TaxID=1313;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC BAA-334 / TIGR4;		
RA	MEDLINE=21357209; PubMed=11463916;		
RA	Tetelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,		
RA	Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,		
RA	Durkin A.S., Winn M., Kolonay J.F., Nelson W.C., Peterson J.D.,		
RA	Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,		
RA	Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,		
RA	McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,		
RA	Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,		
RA	Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;		
RT	"Complete genome sequence of a virulent isolate of Streptococcus pneumoniae."		
RL	Science 293:498-506(2001).		
DR	EMBL; AE007326; AAK74284.1; -.		
DR	PIR; C95011; C95011.		
DR	TIGR; SP0097; -.		
KW	Complete proteome.		
SQ	SEQUENCE 354 AA; 40330 MW; 31130B129C6C1D3A CRC64;		

Query Match 50.0%; Score 52.5; DB 16; Length 354;
Best Local Similarity 66.7%; Pred. No. 8.7;
Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 RMKWKKTALD-WSWL 15

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Db      141 RDKWKEQVLDWFWSL 155
||||: |||||
RESULT 2
ID      Q8CZC0 PRELIMINARY; PRT; 354 AA.
AC      Q8CZC0;
DT      01-WAR-2003 (TrEMBLrel. 23, Created)
DT      01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DE      Hypothetical protein.
GN      SP00086.
OS      Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC      Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC      Streptococcus.
OX      NCBI_TaxID=171101;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21429245; PubMed=11544234;
RA      Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA      DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA      Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA      LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA      McAhren S.M., McHenry M., Mcleaster K., Mundy C.W., Niclas T.I.,
RA      Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
RA      Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA      Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA      Glass J.I.;
RT      "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL      J. Bacteriol. 183:5709-5717(2001).
DR      EMBL; AE008392; AAK98890.1; -.
DR      PIR; F97882; F97882.
KW      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 354 AA; 40335 MW; 0BB6E28E7B4A0690 CRC64;

Query Match      50.0%; Score 52.5; DB 16; Length 354;
Best Local Similarity 66.7%; Pred. No. 8.7;
Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      2 RMKWKTALD-WSWL 15
||||: |||||
Db      141 RDKWKEQVLDWFWSL 155

RESULT 3
ID      Q95KV0 PRELIMINARY; PRT; 756 AA.
AC      Q95KV0;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Ikb kinase-beta.
GN      BIKKBETA.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT      "Identification and characterisation of the bovine Ikb kinases (IKKS)
RT      alpha, beta and gamma.";
RL      Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR      EMBL; AJ414556; CAC93687.1; -.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR000719; Prot_kinase.

Query Match      47.6%; Score 50; DB 5; Length 1208;
Best Local Similarity 52.9%; Pred. No. 71;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      1 RRMKWKKTALDWSWLQ 17
||||: |||||
Db      228 RRPWKYDQADWSHFQT 244

RESULT 5
ID      Q98J62 PRELIMINARY; PRT; 389 AA.
AC      Q98J62;
DT      01-OCT-2001 (TrEMBLrel. 18, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      Hypothetical protein mlr2085.
GN      MLR2085.
OS      Rhizobium loti (Mesorhizobium loti).

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OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MAF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
RL ENBL; AP002998; BAB49304.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 389 AA; 43172 MW; 193288500BFD35 CRC64;

Query Match 46.7%; Score 49; DB 16; Length 389;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 RRMKWKKTALDWSWL 15
Db 128 RRPKGGRAARTWFWL 142

RESULT 6
Q8ZS87
ID Q8ZS87 PRELIMINARY; PRT; 588 AA.
AC Q8ZS87;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein All7625.
GN ALL7625.
OS Anabaena sp. (strain PCC 7120).
OG Plasmid pCC7120beta.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
RL ENBL; AP003602; BAB77268.1; -.
DR PIR; AF2542; AF2542.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 588 AA; 67189 MW; F979CC95145D197B CRC64;

Query Match 46.7%; Score 49; DB 16; Length 588;
Best Local Similarity 54.5%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 WKKTALDWSWL 15
Db 40 WKQEGLDWGWV 50

RESULT 7
Q9XYT7
ID Q9XYT7 PRELIMINARY; PRT; 274 AA.
AC Q9XYT7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Scx-3 homeodomain protein (Fragment).
GN SCOX-3.
OS Cassiopea xamachana.
OC Eukaryota; Metazoa; Chnidaria; Scyphozoa; Rhizostomeae; Cassiopeidae;
OC Cassiopea.
OX NCBI_TaxID=12993;
RN [1]
RP SEQUENCE FROM N.A.
RX Kuhn K., Streit B., Schierwater B.;
RT "Isolation of Hox genes from the scyphozoan Cassiopeia xamachana:
RT Implications for the early evolution of Hox genes."
RL J. Exp. Zool. 0:0-0(1999).
CC 1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR ENBL; AF124593; RAD32577.1; -.
DR HSSP; P02833; 9ANT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
SQ SEQUENCE 274 AA; 31041 MW; 58E91F6E540C3A9 CRC64;

Query Match 46.2%; Score 48.5; DB 5; Length 274;
Best Local Similarity 52.4%; Pred. No. 26;
Matches 11; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 1 RRMKWKKTALDWSWL 18
Db 192 RRMKWKKTGTSIDANELERE 212

RESULT 8
Q07806
ID Q07806 PRELIMINARY; PRT; 251 AA.
AC Q07806;
DT 01-JUN-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphotransferase (Aminoglycoside 3'-phosphotransferase).
GN RV3817 OR MTCY409.13C OR MT3925.1.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H37Rv.
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy J.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CDC 1551 / Oshkosh;
RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

```

RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97188; CAB10016.1; -;
DR EMBL; AE007186; AAK48292.1; -;
DR PIR; E70521; E70521.
DR TIGR; MT3925; -;
DR TubercuList; Rv3817; -;
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR002575; APH.
DR Pfam; PF01636; APH; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 251 AA; 27241 MW; 52807FDA006A21B3 CRC64;
Query Match 45.7%; Score 48; DB 16; Length 251;
Best Local Similarity 30.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 5; Indels 12; Gaps 1;
QY 1 RRMKWKKTAL-----DWSWLQTE 18
Db 64 RRLRWAAPYLAIVPRVLGVGVDGDMWLHTD 93
RESULT 9
Q7TVL6 PRELIMINARY; PRT; 251 AA.
AC Q7TVL6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Putative phosphotransferase (EC 2.7.-).
GN MB3847.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97; PubMed=12788972;
RX MEDLINE=22709107;
RA Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
FL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248347; CAD96033.1; -;
KW Transferase; Complete proteome.
SQ SEQUENCE 251 AA; 27241 MW; 52E07FDA006A21B3 CRC64;
Query Match 45.7%; Score 48; DB 16; Length 251;
Best Local Similarity 30.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 5; Indels 12; Gaps 1;
QY 1 RRMKWKKTAL-----DWSWLQTE 18
Db 64 RRLRWAAPYLAIVPRVLGVGVDGDMWLHTD 93
RESULT 10
Q9AA20 PRELIMINARY; PRT; 549 AA.
ID Q9AA20;
AC Q9AA20;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Hypothetical protein CC0788.
GN CC0788.
OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feidlyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamachavan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005754; AAK22773.1; -;
DR PIR; A87347; A87347.
DR TIGR; CC0788; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 549 AA; 59936 MW; A9A4C53BAED2CC9F CRC64;
Query Match 45.7%; Score 48; DB 16; Length 549;
Best Local Similarity 53.8%; Pred. No. 63;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 KWKKTALDWSWLQ 16
Db 447 KWQFGASDWTWLK 459
RESULT 11
Q26729 PRELIMINARY; PRT; 643 AA.
ID Q26729;
AC Q26729;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MTH632.
GN MTH632.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadator R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000844; AAB85138.1; -;
DR PIR; B69184; B69184.
DR InterPro; IPR002173; pfkB.
DR Pfam; PF00294; pfkB; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 643 AA; 72697 MW; 2FC8E6C6D2FF2E1F CRC64;
Query Match 45.7%; Score 48; DB 17; Length 643;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 RRMKWKKTALDWSW 14
Db 187 RRLSWERTAEFDIW 200

RESULT 12

Q8NMH7 PRELIMINARY; PRT; 706 AA.
 AC Q8NMH7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Protease II.
 GN CGL2596.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005282; BAB99989.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004287; F:prolyl oligopeptidase activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001375; Peptidase S9.
 DR InterPro; IPR004106; Peptidase_S9A_N.
 DR InterPro; IPR000379; Ser_estr8.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF00326; Peptidase_S9; 1.
 DR Pfam; PF02897; Peptidase_S9_N; 1.
 DR PRINTS; PR00862; PROLIGOPTASE.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 706 AA; 78920 MW; 852BB993B6BC5FE4 CRC64;

Query Match 45.7%; Score 48; DB 16; Length 706;
 Best Local Similarity 46.7%; Pred. No. 81;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RRMKKKTALDWSWL 15

Db 683 RYKRWETAFYGYWL 697

RESULT 13

Q7UL36 PRELIMINARY; PRT; 833 AA.
 AC Q7UL36;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative subtilisin proteinase-like protein.
 GN RB9765.
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Glockner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; EX294150; CAD76442.1; -.
 KW Complete proteome.

SQ SEQUENCE 833 AA; 92655 MW; 891EB67CAB5B2624 CRC64;

Query Match 45.7%; Score 48; DB 16; Length 833;
 Best Local Similarity 60.0%; Pred. No. 96;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 WKKTALDWSW 14

Db 499 WSRTPALPNW 508

RESULT 14

Q8F9T9 PRELIMINARY; PRT; 426 AA.
 AC Q8F9T9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative outer membrane protein.
 GN LA0100.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE011201; AAN47299.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR GO; GO:0006281; P:DNA repair; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR InterPro; IPR000977; DNA_ligase.
 DR PROSITE; PS00697; DNA_LIGASE_A1; 1.
 KW Complete proteome.
 SQ SEQUENCE 426 AA; 48025 MW; A1F0B0D76D5F75EF CRC64;

Query Match 45.2%; Score 47.5; DB 16; Length 426;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 8; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 3 MKKKKTALDWSW 14

Db 139 MKKK--EWSW 147

RESULT 15

Q96GH8 PRELIMINARY; PRT; 100 AA.
 AC Q96GH8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to BarH-like homeobox 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; BC009458; AA09458.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH lambrepressr.
 DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 100 AA; 11481 MW; 9F56D9D47A57C69C CRC64;

Query Match 44.8%; Score 47; DB 4; Length 100;
Best Local Similarity 52.9%; Pred. No. 16;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 RRMKWKKTALDWSWLT 17
|||
Db 39 RRMKWKKIVLQGGLES 55

Search completed: September 29, 2004, 16:56:20
Job time : 117 secs